**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

Claim 1 (currently amended): A method for identifying a compound that inhibits transmission of HIV to a target cell, the method comprising contacting synthetic peptide comprising trimers in the presence of a compound and with HR2 peptide under conditions and for a time sufficient to allow formation of a complex between the synthetic peptide comprising trimers and HR2 peptide *in vitro*; and detecting the amount of complex formed; wherein inhibition or reduction of complex formation in the presence of the compound, as compared to complex formation in the absence of the compound, is indicative of ability of the compound to inhibit transmission of HIV to a target cell; and

wherein synthetic peptide comprises an amino acid sequence of more than ~~16~~ 36 amino acid residues and fewer than 60 amino acid residues in length derived from the HR1 region of HIV-1 gp41; wherein the HR1 region consists of ~~native~~ amino acid sequence as shown ~~as~~ in SEQ ID NO:1 or a polymorphism occurring in one or more amino acid residues of such sequence as shown in FIG. 2; wherein the HR1 region from which the synthetic peptide is derived comprises a hydrophobic domain of amino acids corresponding to amino acid residues in positions 28 to 36 of SEQ ID NO:1 or polymorphisms thereof; wherein the amino acid residues comprising the hydrophobic domain correspond to heptad repeat positions "efgabcdef"; and wherein the amino acid sequence of the synthetic peptide further comprises one or more amino acid substitutions in the heptad repeat positions "efgabcdef" comprising the hydrophobic domain, as compared to the ~~native~~ amino acid sequence of ~~the HR1 region~~ SEQ ID NO:1, which enables synthetic peptide to self-assemble in solution into trimers.

Claim 2 (original): The method according to claim 1, wherein the amino acid sequence of the synthetic peptide comprises one or more amino acid substitutions in the hydrophobic domain comprising either a substitution in the "c" position, or a substitution in both the "g" position and the "c" position, of the heptad repeat positions "efgabcdef".

Claim 3 (currently amended): The method according to claim 2, wherein the synthetic peptide comprises ~~an~~ a further amino acid substitution ~~additional~~ in addition to a substitution in either the "c" position or both the "g" position and "c" position, wherein the ~~additional~~ further amino acid substitution is in one or more amino acid positions of one or more heptads of the synthetic peptide, and wherein the one or more amino acid positions is selected from the group consisting of an "a" position, a "d" position, a "b" position, and a combination thereof.

Claim 4 (currently amended): The method according to claim 1, wherein the amino acid sequence of the synthetic peptide comprises one or more amino acid substitutions in the hydrophobic domain comprising the heptad repeat positions ~~"efgabcdef"~~ "$e_1f_2g_3a_4b_5c_6d_7e_8f_9$" that are in a position of the heptad repeat positions selected from the group consisting of ~~a C-terminal "e"~~ an "$e_8$" position, ~~a C-terminal "f"~~ an "$f_9$" position, and a combination thereof.

Claim 5 (currently amended): The method according to claim 4, wherein the synthetic peptide comprises ~~an~~ a further amino acid substitution ~~additional~~ in addition to the substitution in one or more of the ~~"e"~~ "$e_8$" position and the ~~"f"~~ "$f_9$" position, wherein the ~~additional~~ further amino acid substitution is in one or more amino acid positions of one or more heptads of the synthetic peptide, and wherein the one or more amino acid positions is selected from the group consisting of the "a" position, a "d" position, a "b" position, and a combination thereof.

Claim 6 (currently amended): The method according to claim 1, wherein the synthetic peptide further comprises a component selected from the group consisting of one or more ~~reactive functionalities~~ chemical group or moiety capable of forming a covalent bond or protective group, a macromolecular carrier, a pharmaceutically acceptable carrier, an amino acid ~~substitution~~ modification comprising an addition of no less than one amino acid and no more than twenty amino acids to either or both of the amino terminus or carboxy terminus of the synthetic peptide, and a combination thereof.

Claim 7 (original): The method according to claim 1, wherein the synthetic peptide is predominately in trimeric form.

Claim 8 (original): The method according to claim 1, wherein the synthetic peptide is in a monomer-trimer equilibrium.

Claims 9-16 (canceled)

Claim 17 (currently amended): In a method for identifying or producing a molecule that can inhibit the binding between HR1 and HR2 regions of HIV gp41, the improvement which comprises: use of a trimer as a binding partner with HR2 peptide in detecting *in vitro* the ability of the molecule to bind to an HR (heptad repeat) region of HIV gp41; wherein the trimer is comprised of synthetic peptide comprising an amino acid sequence of more than ~~16~~ 36 amino acid residues and fewer than 60 amino acid residues in length derived from the HR1 region of HIV-1 gp41; wherein the HR1 region consists of ~~native~~ amino acid sequence as shown ~~as~~ in SEQ ID NO:1 or a polymorphism occurring in one or more amino acid residues of such sequence as shown in FIG. 2; wherein the HR1 region from which the synthetic peptide is derived comprises a hydrophobic domain of amino acids corresponding to amino acid residues in positions 28 to 36 of SEQ ID NO:1 or polymorphisms thereof; wherein the amino acid residues comprising the hydrophobic domain correspond to heptad repeat positions "efgabcdef"; and wherein the amino acid sequence of the synthetic peptide further comprises one or more amino acid substitutions in the heptad repeat positions "efgabcdef" comprising the hydrophobic domain, as compared to the ~~native~~ amino acid sequence of ~~the HR1 region~~ SEQ ID NO:1, which enables synthetic peptide to self-assemble in solution into trimers.

Claim 18 (original): The method according to claim 17, wherein the amino acid sequence of the synthetic peptide comprises one or more amino acid substitutions in the hydrophobic domain comprising either a substitution in the "c" position, or a substitution in both the "g" position and the "c" position, of the heptad repeat positions "efgabcdef".

Claim 19 (currently amended): The method according to claim 18, wherein the synthetic peptide comprises ~~an~~ a further amino acid substitution ~~additional~~ in addition to a substitution in either the "c" position or both the "g" position and "c" position, wherein the ~~additional~~ further amino acid substitution is in one or more amino acid positions of one or more heptads of the synthetic peptide, and wherein the one or more amino acid positions is

selected from the group consisting of an "a" position, a "d" position, a "b" position, and a combination thereof.

Claim 20 (currently amended): The method according to claim 17, wherein the amino acid sequence of the synthetic peptide comprises one or more amino acid substitutions in the hydrophobic domain comprising the heptad repeat positions ~~"efgabcdef"~~ "$e_1f_2g_3a_4b_5c_6d_7e_8f_9$" that are in a position of the heptad repeat positions selected from the group consisting of ~~a C-terminal "e"~~ an "$e_8$" position, ~~a C-terminal "f"~~ an "$f_9$" position, and a combination thereof.

Claim 21 (currently amended): The method according to claim 20, wherein the synthetic peptide comprises ~~an~~ a further amino acid substitution ~~additional~~ in addition to the substitution in one or more of the ~~"e"~~ "$e_8$" position and the ~~"f"~~ "$f_9$" position, wherein the ~~additional~~ further amino acid substitution is in one or more amino acid positions of one or more heptads of the synthetic peptide, and wherein the one or more amino acid positions is selected from the group consisting of the "a" position, a "d" position, a "b" position, and a combination thereof.

Claim 22 (currently amended): The method according to claim 17, wherein the synthetic peptide further comprising a component selected from the group consisting of one or more ~~reactive functionalities~~ chemical group or moiety capable of forming a covalent bond or protective group, a macromolecular carrier, a pharmaceutically acceptable carrier, an amino acid ~~substitution~~ modification comprising an addition of no less than one amino acid and no more than twenty amino acids to either or both of the amino terminus or carboxy terminus of the synthetic peptide, and a combination thereof.

Claim 23 (currently amended): A method for identifying a compound that inhibits transmission of HIV to a target cell, the method comprising contacting synthetic peptide comprising trimers in the presence of a compound and with HR2 peptide under conditions and for a time sufficient to allow formation of a complex between the synthetic peptide comprising trimers and HR2 peptide *in vitro*; and detecting the amount of complex formed; wherein inhibition or reduction of complex formation in the presence of the compound, as

compared to complex formation in the absence of the compound, is indicative of ability of the compound to inhibit transmission of HIV to a target cell; and

wherein synthetic peptide comprises an amino acid sequence of more than ~~16~~ 36 amino acid residues and fewer than 60 amino acid residues in length containing ~~native~~ sequence of the HR1 region of HIV-1 gp41 as shown in SEQ ID NO:1; wherein the HR1 region sequence comprises a hydrophobic domain of amino acids corresponding to amino acid residues in positions 28 to 36 of SEQ ID NO:1; wherein the amino acid residues comprising the hydrophobic domain correspond to heptad repeat positions "efgabcdef"; and wherein the amino acid sequence of the synthetic peptide further comprises one or more amino acid substitutions in the heptad repeat positions "efgabcdef" comprising the hydrophobic domain, as compared to the ~~native~~ amino acid sequence of ~~the HR1 region~~ SEQ ID NO:1, which enables synthetic peptide to self-assemble in solution into trimers.

Claim 24 (currently amended): In a method for identifying or producing a molecule that can inhibit the binding between HR1 and HR2 regions of HIV gp41, the improvement which comprises: use of a trimer as a binding partner with HR2 peptide in detecting *in vitro* the ability of the molecule to bind to an HR (heptad repeat) region of HIV gp41;
wherein the trimer is comprised of synthetic peptide comprising an amino acid sequence of more than ~~16~~ 36 amino acid residues and fewer than 60 amino acid residues in length containing ~~native~~ sequence of the HR1 region of HIV-1 gp41 as shown in SEQ ID NO:1; wherein the HR1 region sequence comprises a hydrophobic domain of amino acids corresponding to amino acid residues in positions 28 to 36 of SEQ ID NO:1; wherein the amino acid residues comprising the hydrophobic domain correspond to heptad repeat positions "efgabcdef"; and wherein the amino acid sequence of the synthetic peptide further comprises one or more amino acid substitutions in the heptad repeat positions "efgabcdef" comprising the hydrophobic domain, as compared to the ~~native~~ amino acid sequence of ~~the HR1 region~~ SEQ ID NO:1, which enables synthetic peptide to self-assemble in solution into trimers.